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H S C  
SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANTS: NATHAN A. ELLIS, JAMES GERMAN, AND JOANNA GRODEN

(ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF BLOOM'S SYNDROME

(iii) NUMBER OF SEQUENCES: 78

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN  
(B) STREET: 90 PARK AVENUE  
(C) CITY: NEW YORK  
(D) STATE: NEW YORK  
(E) COUNTRY: U.S.A.  
(F) ZIP: 10016

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE DISKETTE  
(B) COMPUTER: IBM PC COMPATIBLE  
(C) OPERATING SYSTEM: MS-DOS  
(D) SOFTWARE: ASCII

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/559,303  
(B) FILING DATE: NOVEMBER 15, 1995

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: ELIZABETH A. BOGOSIAN  
(B) REGISTRATION NUMBER: 39,911  
(C) REFERENCE/DOCKET NUMBER: 63475/65

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (212) 697-5995  
(B) TELEFAX: (212) 286-0854 or 286-0082  
(C) TELEX: TWX 710-581-4766

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1  
GGTGGCGACG ACTCCTGGA 19

(3) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2  
ACCAGACCAA CTGGTAATG 19

(4) INFORMATION FOR SEQ ID NO: 3

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3

ATGGTAGCGA CCGGCGCTCA 20

(5) INFORMATION FOR SEQ ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

CCGTCAGTAT CGGCGGAATT 20

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

4  
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(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

TTGTGGTGTT GGGTAGAGGT T 21

(7) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

GCCGCCGGCA CCAAC 15

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7  
CCTCAGTCAA ATCTATNTGC TC 22

(9) INFORMATION FOR SEQ ID NO: 8

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8  
GCCATCACCG GAACAGAAAGG AAA 23

(10) INFORMATION FOR SEQ ID NO: 9

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9

TCTTCTGGAG GAGGTGGAAC AA 22

(11) INFORMATION FOR SEQ ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10

GGATCCTGGT TCCGTCCGC 19

(12) INFORMATION FOR SEQ ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11

CAACTAGAAC GTCACTCAGC C 21

(13) INFORMATION FOR SEQ ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12

GACTTTCCCT TCAGTGAAACC TC 22

(14) INFORMATION FOR SEQ ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13

CCAGATTCT TGCAGACTCC G 21

(15) INFORMATION FOR SEQ ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14

CTTAAAGTAC CATCAATGAT TGGG 24

(16) INFORMATION FOR SEQ ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:

(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15

GAGTAAGCAC TGCTCAGAAA TC 22

(17) INFORMATION FOR SEQ ID NO: 16

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16

CGAGCAAATA GATTTGACTG AGG 23

(18) INFORMATION FOR SEQ ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17

GAAGATGCTC AGGAAAGTGA C 21

(19) INFORMATION FOR SEQ ID NO: 18

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

- (iii) HYPOTHETICAL: YES

- (iv) ANTI-SENSE: NO

- (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18

CAACTGAGAA AGTTCCATGT ATTG 24

(20) INFORMATION FOR SEQ ID NO: 19

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

- (iii) HYPOTHETICAL: YES

- (iv) ANTI-SENSE: NO

- (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19

CTATTCCTGA TGATAAACTG AAAC 24

(21) INFORMATION FOR SEQ ID NO: 20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20

GTGGAGATAc AGGCCTGATT C 21

(22) INFORMATION FOR SEQ ID NO: 21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21

CAGGATTCTC TGCCACCAGG 20

(23) INFORMATION FOR SEQ ID NO: 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22

CAGGAAATGT TCTCACAAAGC AC 22

(24) INFORMATION FOR SEQ ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23

CAGCCAGCAA ATCTTCCACA G 21

(25) INFORMATION FOR SEQ ID NO: 24

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24

GAATTATACT GACAAGTCAG CAC 23

(26) INFORMATION FOR SEQ ID NO: 25

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25

CTCCTGGGGT CACTGTTGTC 20

(27) INFORMATION FOR SEQ ID NO: 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26

GAGGTTCACT GAAGGAAAAG TC 22

(28) INFORMATION FOR SEQ ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27

GAAGTCCTTG ACCCTTGCT G 21

(29) INFORMATION FOR SEQ ID NO: 28

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28

GGGATTCTT TACAGTTGGT GTG 23

(30) INFORMATION FOR SEQ ID NO: 29

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29

CTCTTACAAA GTGACTTTGG GG 22

(31) INFORMATION FOR SEQ ID NO: 30

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30

CCTCAGTCAA ATCTATTG C TCG 23

(32) INFORMATION FOR SEQ ID NO: 31

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31

GCTTAACCAT TCTGAGTCAT CC 22

(33) INFORMATION FOR SEQ ID NO: 32

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32  
CAATACATGG AACTTTCTCA GTTG 24

(34) INFORMATION FOR SEQ ID NO: 33

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33  
CGTACTAAGG CATTGTGAAG AGG 23

(35) INFORMATION FOR SEQ ID NO: 34

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

CACAGTCTGT GCTGGTTCT G 21

(36) INFORMATION FOR SEQ ID NO: 35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35

CCTTCATAGA ATTCCCTGTA GG 22

(37) INFORMATION FOR SEQ ID NO: 36

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36

GTGTTTCAGC CCAGTTGCTA C 21

(38) INFORMATION FOR SEQ ID NO: 37

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

GCAGTATGTT TATTCTGATC TTTC 24

(39) INFORMATION FOR SEQ ID NO: 38

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38

CCTTGATGGG TTGATAGGCA G 21

(40) INFORMATION FOR SEQ ID NO: 39

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

CGCTCATGTT TCAGATTCT GG 22

(41) INFORMATION FOR SEQ ID NO: 40

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40

GATCTACGAT AAGTGATCTC AAG 23

(42) INFORMATION FOR SEQ ID NO: 41

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41

GAGTCTGTTA CTTGCACAGA TC 22

(43) INFORMATION FOR SEQ ID NO: 42

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42

CAATCATAAA ACTTCTATAT GTCAC 25

(44) INFORMATION FOR SEQ ID NO: 43

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43

GTGGGGACAT GATTTTCGTC AAG 23

(45) INFORMATION FOR SEQ ID NO: 44

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44

GACATCCTGA CTCAGCTGAA G 21

(46) INFORMATION FOR SEQ ID NO: 45

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45

GCACCACCCA TATGATTCA G 21

(47) INFORMATION FOR SEQ ID NO: 46

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46

GATGAAGTGC AGCAGAAGTG G 21

(48) INFORMATION FOR SEQ ID NO: 47

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47

GCAGAGCTGG AAGAGATGGG 20

(49) INFORMATION FOR SEQ ID NO: 48

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48

GTATAGCATG GTACATTACT GTG 23

(50) INFORMATION FOR SEQ ID NO: 49

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49

GACTGACGAT GTGAAAAGTA TTG 23

(51) INFORMATION FOR SEQ ID NO: 50

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50

CCAGTCAGGT ATATTTGGAA AAG 23

(52) INFORMATION FOR SEQ ID NO: 51

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51

CGATCGCTTA TGTGATGCTC G 21

(53) INFORMATION FOR SEQ ID NO: 52

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52

GAACTTACAG AAGTCTGCAA ATC 23

(54) INFORMATION FOR SEQ ID NO: 53

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53

GGTGTTACTG AAGACAACT GG 22

(55) INFORMATION FOR SEQ ID NO: 54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54

GGATAAGCCT GTCCAGCAGC 20

(56) INFORMATION FOR SEQ ID NO: 55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55

GCTTCCAGTG GTTCCAAGGC 20

(57) INFORMATION FOR SEQ ID NO: 56

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56

CTCAAGCGAC ATCAGGAGCC 20

(58) INFORMATION FOR SEQ ID NO: 57

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57

GCCATCACCG GAACAGAAGG 20

(59) INFORMATION FOR SEQ ID NO: 58

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58

GATTATGTCT GTTAAAGCTC ATG 23

(60) INFORMATION FOR SEQ ID NO: 59

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59

CGTGTCAAGCC ATGGTGTCAC 20

(61) INFORMATION FOR SEQ ID NO: 60

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60

CAGATAACCT GACAGCCATC C 21

(62) INFORMATION FOR SEQ ID NO: 61

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61

CAGTCTGGTC ACATCATGAT AG 22

(63) INFORMATION FOR SEQ ID NO: 62

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62

GCTGTATTCT CCTGCATTCC G 21

(64) INFORMATION FOR SEQ ID NO: 63

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63

CCTTGTGATG AACTATGTTTC TTG 23

(65) INFORMATION FOR SEQ ID NO: 64

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64

CCAAAATCTT GTCAAGTATC AGC 23

(66) INFORMATION FOR SEQ ID NO: 65

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65

GGAATTTCTT GTTTCCATAA AGTC 24

(67) INFORMATION FOR SEQ ID NO: 66

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66

CAAGCTTCTT GAGAGTGACG G 21

(68) INFORMATION FOR SEQ ID NO: 67

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67

GATGTCCATT CAGAGTATTT CTG 23

(69) INFORMATION FOR SEQ ID NO: 68

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68

GGGTATTCC TCGTCAAGCT C 21

(70) INFORMATION FOR SEQ ID NO: 69

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69

CCTAGATATC TTTCTACATG TGG 23

(71) INFORMATION FOR SEQ ID NO: 70

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70

GTTATGAGAA TGCATATGAA GGC 23

(72) INFORMATION FOR SEQ ID NO: 71

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24
  - (B) TYPE: NUCLEIC ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY:
  - (B) LOCATION:
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71

CAAGAATAAAC AGCTTTATAG TCAC 24

(73) INFORMATION FOR SEQ ID NO: 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4437
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72

GC	CG	GG	CG	GC	CGTGGTTGCG	GCGCGGGAAG	TTTGGATCCT	GGTTCCGTCC	GCTAGGAGTC	60
TG	CG	TG	CAG	GATTATGGCT	GCTGTCCTC	AAAATAATCT	ACAGGAGCAA	CTAGAACGTC		120
A	CT	CAG	CC	AG	AACACTTAAT	AATAAAATTAA	GTCTTCAAA	ACCAAAATT	TCAGGTTCA	180
C	TT	TT	AA	AA	CTTTAAAAAA	GAAAACATCT	TCAGATAACA	ATGTATCTGT	AACTAATGTG	240
A	AA	AC	CT	GT	AAACACCTGT	ATTAAGAAAT	AAAGATGTTA	ATGTTACCGA	AGACTTTCC	300
C	CT	TAC	CC	AA	CTCTACCCAA	CACCACAAAT	CAGCAAAGGG	TCAAGGACTT	TTCAAGTGAAC	360
G	AC	AG	AA	AC	GACAGGAAAC	ACAGAGAGGT	GGATCAAAT	CATTATTGCC	AGATTCTTG	420
A	GG	AG	TT	GT	AGGAAGTTGT	ATGCACTACC	CAAAACACAC	CAACTGTAAA	GAAATCCC GG	480
T	CA	AA	TT	AG	TCAAGAAATT	AGAATTTAGT	TCTTCACCAAG	ATTCTTAAG	TACCATCAAT	540
A	AT	GG	AT	GA	ATATGGATGA	CTTTGATACT	TCTGAGACTT	CAAAATCATT	TGTTACACCA	600
C	TT	AA	AC	AC	ACTTTGTAAG	AGTAAGCACT	GCTCAGAAAT	CAAAAAAGGG	TAAGAGAAAC	660
A	AC	AA	AC	AC	CACAGCTTTA	TACAACAAAC	ACAGTAAAGA	CTGATTTGCC	TCCACCCCTCC	720
G	AA	AT	AG	GAG	AGCAAATAGA	TTTGACTGAG	GAACAGAAGG	ATGACTCAGA	ATGGTTAAGC	780
T	TT	GC	CAT	CG	TTTGACATCGA	TGATGGCCCC	ATTGCTGAAG	TGCATATAAA	TGAAGATGCT	840
A	CT	CT	GT	AA	ACTCTCTGAA	AACTCATTG	GAAGATGAAA	GAGATAATAG	CGAAAAGAAG	900

AAGAAGCTGA ATTACATTCA ACTGAGAAAG TTCCATGTAT TGAATTTGAT GATGATGATT 960  
ATGATAACGGA TTTTGTCCA CCTTCTCCAG AAGAAATTAT TTCTGCTTCT TCTTCCTCTT 1020  
CAAAATGCCT TACTACGTTA AAGGACCTTG ACACATCTGA CAGAAAAGAG GATGTTCTTA 1080  
GCACATCAAA AGATCTTTG TCAAAAACCTG AGAAAATGAG TATGCAGGAG CTGAATCCAG 1140  
AAACCAGCAC AGACTGTGAC GCTAGACAGA TAAGTTACA GCAGCAGCTT ATTCATGTGA 1200  
TGGAGCACAT CTGTAAATTA ATTGATACTA TTCCTGATGA TAAACTGAAA CTTTGGATT 1260  
GTGGGAACGA ACTGCTTCAG CAGCGGAACA TAAGAAGGAA ACTTCTAACG GAAGTAGATT 1320  
TTAATAAAAG TGATGCCAGT CTTCTGGCT CATTGTGGAG ATACAGGCCT GATTCACTTG 1380  
ATGGCCCTAT GGAGGGTGAT TCCTGCCCTA CAGGGATTTC TATGAAGGAG TTAAATTTT 1440  
CACACCTTCC CTCAAATTCT GTTTCTCCTG GGGACTGTTT ACTGACTACC ACCCTAGGAA 1500  
AGACAGGATT CTCTGCCACC AGGAAGAAC CTTTGAAAG GCCTTTATTC AATACCCATT 1560  
TACAGAAGTC CTTTGTAAAGT AGCAACTGGG CTGAAACACC AAGACTAGGA AAAAAAAATG 1620  
AAAGCTCTTA TTTCCCAGGA AATGTTCTCA CAAGCACTGC TGTGAAAGAT CAGAATAAAC 1680  
ATACTGCTTC AATAAATGAC TTAGAAAGAG AAACCCAACC TTCTATGAT ATTGATAATT 1740  
TTGACATAGA TGACTTTGAT GATGATGATG ACTGGGAAGA CATAATGCAT AATTAGCAG 1800  
CCAGCAAATC TTCCACAGCT GCCTATCAAC CCATCAAGGA AGGTCGGCCA ATTAAATCAG 1860  
TATCAGAAAG ACTTTCTCA GCCAAGACAG ACTGTCTTCC AGTGTCTACT ACTGCTAAA 1920  
ATATAAAACTT CTCAGAGTCA ATTCAAGATT ATACTGACAA GTCAGCACAA AATTAGCAT 1980  
CCAGAAATCT GAAACATGAG CGTTTCCAAA GTCTTAGTTT TCCTCATACA AAGGAAATGA 2040  
TGAAGATTTT TCATAAAAAA TTTGGCCTGC ATAATTTAG AACTAATCAG CTAGAGGCGA 2100  
TCAATGCTGC ACTGCTTGGT GAAGACTGTT TTATCCTGAT GCCGACTGGA GGTGGTAAGA 2160  
GTTTGTGTTA CCAGCTCCCT GCCTGTGTTT CTCCTGGGGT CACTGTTGTC ATTTCTCCCT 2220  
TGAGATCACT TATCGTAGAT CAAGTCCAAA AGCTGACTTC CTTGGATATT CCAGCTACAT 2280  
ATCTGACAGG TGATAAGACT GACTCAGAAG CTACAAATAT TTACCTCCAG TTATCAAAAA 2340  
AAGACCCAAT CATAAAACTT CTATATGTCA CTCCAGAAAA GATCTGTGCA AGTAACAGAC 2400  
TCATTTCTAC TCTGGAGAAT CTCTATGAGA GGAAGCTCTT GGCACGTTT GTTATTGATG 2460

AAGCACATTG TGTCAGTCAG TGGGGACATG ATTTTCGTCA AGATTACAAA AGAATGAATA 2520  
TGCTTCGCCA GAAGTTTCCT TCTGTTCCGG TGATGGCTCT TACGGCCACA GCTAATCCCA 2580  
GGGTACAGAA GGACATCCTG ACTCAGCTGA AGATTCTCAG ACCTCAGGTG TTTAGCATGA 2640  
GCTTTAACAG ACATAATCTG AAATACTATG TATTACCGAA AAAGCCTAAA AAGGTGGCAT 2700  
TTGATTGCCT AGAATGGATC AGAAAGCACC ACCCATATGA TTCAGGGATA ATTTACTGCC 2760  
TCTCCAGGCG AGAATGTGAC ACCATGGCTG ACACGTTACA GAGAGATGGG CTCGCTGCTC 2820  
TTGCTTACCA TGCTGGCCTC AGTGATTCTG CCAGAGATGA AGTGCAGCAG AAGTGGATTA 2880  
ATCAGGATGG CTGTCAGGTT ATCTGTGCTA CAATTGCATT TGGAAATGGGG ATTGACAAAC 2940  
CGGACGTGCG ATTTGTGATT CATGCATCTC TCCCTAAATC TGTGGAGGGT TACTACCAAG 3000  
AATCTGGCAG AGCTGGAAGA GATGGGGAAA TATCTCACTG CCTGCTTTTC TATAACCTATC 3060  
ATGATGTGAC CAGACTGAAA AGACTTATAA TGATGGAAAA AGATGGAAAC CATCATACAA 3120  
GAGAAACTCA CTTCAATAAT TTGTATAGCA TGGTACATTA CTGTGAAAAT ATAACGGAAT 3180  
GCAGGAGAAT ACAGCTTTG GCCTACTTTG GTGAAAATGG ATTTAACCT GATTTTGTA 3240  
AGAAACACCC AGATGTTCT TGTGATAATT GCTGTAAAAC AAAGGATTAT AAAACAAGAG 3300  
ATGTGACTGA CGATGTGAAA AGTATTGTA GATTGTTCA AGAACATAGT TCATCACAAG 3360  
GAATGAGAAA TATAAAACAT GTAGGTCCCT CTGGAAGATT TACTATGAAT ATGCTGGTCG 3420  
ACATTTCTT GGGGAGTAAG AGTGCACAAA TCCAGTCAGG TATATTTGGA AAAGGATCTG 3480  
CTTATTCACTG ACACAATGCC GAAAGACTTT TTAAAAAGCT GATACTTGAC AAGATTTGG 3540  
ATGAAGACTT ATATATCAAT GCCAATGACC AGGCGATCGC TTATGTGATG CTCGGAAATA 3600  
AAGCCCCAAC TGTACTAAAT GGCAATTAA AGGTAGACTT TATGGAAACA GAAAATTCCA 3660  
GCAGTGTGAA AAAACAAAAA GCGTTAGTAG CAAAAGTGTG TCAGAGGGAA GAGATGGTTA 3720  
AAAAATGTCT TGGAGAACCT ACAGAAAGTCT GCAAATCTCT GGGGAAAGTT TTTGGTGTCC 3780  
ATTACTTCAA TATTTTAAT ACCGTCACTC TCAAGAAGCT TGCAGAAATCT TTATCTTCTG 3840  
ATCCTGAGGT TTTGCTTCAA ATTGATGGTG TTACTGAAGA CAAACTGGAA AAATATGGTG 3900  
CGGAAGTGAT TTCAGTATTA CAGAAATACT CTGAATGGAC ATGCCAGCT GAAGACAGTT 3960  
CCCCAGGGAT AAGCCTGTCC AGCAGCAGAG GCCCCGGAAG AAGTGCCGCT GAGGAGCTTG 4020

ACGAGGAAAT ACCCGTATCT TCCCACACT TTGCAAGTAA AACCGAGAAAT GAAAGGAAGA 4080  
GGAAAAAGAT GCCAGCCTCC CAAAGGTCTA AGAGGAGAAA AACTGCTTCC AGTGGTTCCA 4140  
AGGCAAAGGG GGGGTCTGCC ACATGTAGAA AGATATCTTC CAAAACGAAA TCCTCCAGCA 4200  
TCATTGGATC CAGTTCAGCC TCACATACTT CTCAAGCGAC ATCAGGAGCC AATAGCAAAT 4260  
TGGGGATTAT GGCTCCACCG AAGCCTATAA ATAGACCGTT TCTTAAGCCT TCATATGCAT 4320  
TCTCATAACA ACCGAATCTC AATGTACATA GACCCTCTT CTTGTTGTC AGCATCTGAC 4380  
CATCTGTGAC TATAAAGCTG TTATTCTTGT TATACCAAAA AAAAAAAA AAAAAAA 4437

(74) INFORMATION FOR SEQ ID NO: 73

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73

GCTTCCGGCG GAAGTGAGCC AGGGCTTGGC GCGGCGGCCG TGGTTGCGGC 50  
GCGGGAAGTT TGGAT 65

(75) INFORMATION FOR SEQ ID NO: 74

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74

Phe Pro His Thr Lys Glu Met Met Lys Ile Phe His Lys Lys Phe  
1 5 10 15

Gly Leu His Asn Phe Arg Thr Asn Gln Leu Glu Ala Ile Asn Ala  
20 25 30

Ala Leu Leu Gly Glu Asp Cys Phe Ile Leu Met Pro Thr Gly Gly  
35 40 45

Gly Lys Ser Leu Cys Tyr Gln Leu Pro Ala Cys Val Ser Pro Gly  
50 55 60

Val Thr Val Val Ile Ser Pro Leu Arg Ser Leu Ile Val Asp Gln  
65 70 75

Val Gln Lys Leu Thr Ser Leu Asp Ile Pro Ala Thr Tyr Leu Thr  
80 85 90

Gly Asp Lys Thr Asp Ser Glu Ala Thr Asn Ile Tyr Leu Gln Leu  
95 100 105

Ser Lys Lys Asp Pro Ile Ile Lys Leu Leu Tyr Val Thr Pro Glu  
110 115 120

Lys Ile Cys Ala Ser Asn Arg Leu Ile Ser Thr Leu Glu Asn Leu  
125 130 135

Tyr Glu-Arg Lys Leu Leu Ala Arg Phe Val Ile Asp Glu Ala His  
140 145 150

Cys Val Ser Gln Trp Gly His Asp Phe Arg Gln Asp Tyr Lys Arg  
155 160 165

Met Asn Met Leu Arg Gln Lys Phe Pro Ser Val Pro Val Met Ala  
170 175 180

Leu Thr Ala Thr Ala Asn Pro Arg Val Gln Lys Asp Ile Leu Thr  
185 190 195

Gln Leu Lys Ile Leu Arg Pro Gln Val Phe Ser Met Ser Phe Asn  
200 205 210

Arg His Asn Leu Lys Tyr Tyr Val Leu Pro Lys Lys Pro Lys Lys  
215 220 225

Val Ala Phe Asp Cys Leu Glu Trp Ile Arg Lys His His Pro Tyr  
230 235 240

Asp Ser Gly Ile Ile Tyr Cys Leu Ser Arg Arg Glu Cys Asp Thr  
245 250 255

Met Ala Asp Thr Leu Gln Arg Asp Gly Leu Ala Ala Leu Ala Tyr  
260 265 270

His Ala Gly Leu Ser Asp Ser Ala Arg Asp Glu Val Gln Gln Lys  
275 280 285

Trp Ile Asn Gln Asp Gly Cys Gln Val Ile Cys Ala Thr Ile Ala  
290 295 300

Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Phe Val Ile His  
305 310 315

Ala Ser Leu Pro Lys Ser Val Glu Gly Tyr Tyr Gln Glu Ser Gly  
320 325 330

Arg Ala Gly Arg Asp Gly Glu Ile Ser His Cys Leu Leu Phe Tyr  
335 340 345

Thr Tyr His Asp Val Thr Arg Leu Lys Arg Leu Ile Met Met Glu  
350 355 360

Lys Asp Gly Asn His His Thr Arg Glu Thr His Phe Asn Asn Leu  
365 370 375

Tyr Ser Met Val His Tyr Cys Glu Asn Ile Thr Glu Cys Arg Arg  
380 385 390

Ile Gln Leu

(76) INFORMATION FOR SEQ ID NO: 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:  
(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:  
(A) NAME/KEY:  
(B) LOCATION:  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75

Phe Pro Trp Ser Gly Lys Val Lys Asp Ile Leu Gln Asn Val Phe  
1 5 10 15

Lys Leu Glu Lys Phe Arg Pro Leu Gln Leu Glu Thr Ile Asn Val  
20 25 30

Thr Met Ala Gly Lys Glu Val Phe Leu Val Met Pro Thr Gly Gly  
35 40 45

Gly Lys Ser Leu Cys Tyr Gln Leu Pro Ala Leu Cys Ser Asp Gly  
50 55 60

Phe Thr Leu Val Ile Cys Pro Leu Ile Ser Leu Met Glu Asp Gln  
65 70 75

Leu Met Val Leu Lys Gln Leu Gly Ile Ser Ala Thr Met Leu Asn  
80 85 90

Ala Ser Ser Ser Lys Glu His Val Lys Trp Val His Asp Glu Met  
95 100 105

Val Asn Lys Asn Ser Glu Leu Lys Leu Ile Tyr Val Thr Pro Glu  
110 115 120

Lys Ile Ala Lys Ser Lys Met Phe Met Ser Arg Leu Glu Lys Ala  
125 130 135

Tyr Glu Ala Arg Arg Phe Thr Arg Ile Ala Val Asp Glu Val His  
140 145 150

Cys Cys Ser Gln Trp Gly His Asp Phe Arg Pro Asp Tyr Lys Ala  
155 160 165

Leu Gly Ile Leu Lys Arg Gln Phe Pro Asn Ala Ser Leu Ile Gly  
170 175 180

Leu Thr Ala Thr Ala Thr Asn His Val Leu Thr Asp Ala Gln Lys  
185 190 195

Ile Leu Cys Ile Glu Lys Cys Phe Thr Phe Thr Ala Ser Phe Asn  
200 205 210

Arg Pro Asn Leu Tyr Tyr Glu Val Arg Gln Lys Pro Ser Asn Thr  
215 220 225

Glu Asp Phe Ile Glu Asp Ile Val Lys Leu Ile Asn Gly Arg Tyr  
230 235 240

Lys Gly Gln Ser Gly Ile Ile Tyr Cys Phe Ser Gln Lys Asp Ser  
245 250 255

Glu Gln Val Thr Val Ser Leu Gln Asn Leu Gly Ile His Ala Gly  
260 265 270

Ala Tyr His Ala Asn Leu Glu Pro Glu Asp Lys Thr Thr Val His  
275 280 285

Arg Lys Trp Ser Ala Asn Glu Ile Gln Val Val Val Ala Thr Val  
290 295 300

Ala Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Phe Val Ile  
305 310 315

His His Ser Met Ser Lys Ser Met Glu Asn Tyr Tyr Gln Glu Ser  
320 325 330

Gly Arg Ala Gly Arg Asp Asp Met Lys Ala Asp Cys Ile Leu Tyr  
335 340 345

Tyr Gly Phe Gly Asp Ile Phe Arg Ile Ser Ser Met Val Val Met  
350 355 360

Glu Asn Val Gly Gln Gln Lys Leu Tyr Glu Met Val Ser Tyr Cys  
365 370 375

Gln Asn Ile Ser Lys Ser Arg Arg Val Leu Met  
380 385

(77) INFORMATION FOR SEQ ID NO: 76

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

(A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76

Tyr	Pro	Trp	Ser	Asp	Glu	Val	Leu	Tyr	Arg	Leu	His	Glu	Val	Phe
1				5					10					15
Lys	Leu	Pro	Gly	Phe	Arg	Pro	Asn	Gln	Leu	Glu	Ala	Val	Asn	Ala
				20				25					30	
Thr	Leu	Gln	Gly	Lys	Asp	Val	Phe	Val	Leu	Met	Pro	Thr	Gly	Gly
				35				40					45	
Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Leu	Pro	Ala	Val	Val	Lys	Ser	Gly
				50				55					60	
Lys	Thr	His	Gly	Thr	Thr	Ile	Val	Ile	Ser	Pro	Leu	Ile	Ser	Leu
				65				70					75	
Met	Gln	Asp	Gln	Val	Glu	His	Leu	Leu	Asn	Lys	Asn	Ile	Lys	Ala
				80				85					90	
Ser	Met	Phe	Ser	Ser	Arg	Gly	Thr	Ala	Glu	Gln	Arg	Arg	Gln	Thr
				95					100					105
Phe	Asn	Leu	Phe	Ile	Asn	Gly	Leu	Leu	Asp	Leu	Val	Tyr	Ile	Ser
				110				115					120	
Pro	Glu	Met	Ile	Ser	Ala	Ser	Glu	Gln	Cys	Lys	Arg	Ala	Ile	Ser
				125				130					135	
Arg	Leu	Tyr	Ala	Asp	Gly	Lys	Leu	Ala	Arg	Ile	Val	Val	Asp	Glu
				140				145					150	
Ala	His	Cys	Val	Ser	Asn	Trp	Gly	His	Asp	Phe	Arg	Pro	Asp	Tyr
				155				160					165	
Lys	Glu	Leu	Lys	Phe	Phe	Lys	Arg	Glu	Tyr	Pro	Asp	Ile	Pro	Met
				170				175					180	
Ile	Ala	Leu	Thr	Ala	Thr	Ala	Ser	Glu	Gln	Val	Arg	Met	Asp	Ile
				185				190					195	

Ile His Asn Leu Glu Leu Lys Glu Pro Val Phe Leu Lys Gln Ser  
200 205 210

Phe Asn Arg Thr Asn Leu Tyr Tyr Glu Val Asn Lys Lys Thr Lys  
215 220 225

Asn Thr Ile Phe Glu Ile Cys Asp Ala Val Lys Ser Arg Phe Lys  
230 235 240

Asn Gln Thr Gly Ile Ile Tyr Cys His Ser Lys Lys Ser Cys Glu  
245 250 255

Gln Thr Ser Ala Gln Met Gln Arg Asn Gly Ile Lys Cys Ala Tyr  
260 265 270

Tyr His Ala Gly Met Glu Pro Asp Glu Arg Leu Ser Val Gln Lys  
275 280 285

Ala Trp Gln Ala Asp Glu Ile Gln Val Ile Cys Ala Thr Val Ala  
290 295 300

Phe Gly Met Gly Ile Asp Lys Pro Asp Val Arg Phe Val Tyr His  
305 310 315

Phe Thr Val Pro Arg Thr Leu Glu Gly Tyr Tyr Gln Glu Thr Gly  
320 325 330

Arg Ala Gly Arg Asp Gly Asp Tyr Ser Tyr Cys Ile Thr Tyr Phe  
335 340 345

Ser Phe Arg Asp Ile Arg Thr Met Gln Thr Met Ile Gln Lys Asp  
350 355 360

Lys Asn Leu Asp Arg Glu Asn Lys Glu Lys His Leu Asn Lys Leu  
365 370 375

Gln Gln Val Met Ala Tyr Cys Asp Asn Val Thr Asp Cys Arg Arg  
380 385 390

Lys Leu Val

(78) INFORMATION FOR SEQ ID NO: 77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: OTHER NUCLEIC ACID

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77

Val	Leu	Gln	Glu	Thr	Phe	Gly	Tyr	Gln	Gln	Phe	Arg	Pro	Gly	Gln
1					5				10					15
Glu	Glu	Ile	Ile	Asp	Thr	Val	Leu	Ser	Gly	Arg	Asp	Cys	Leu	Val
					20				25					30
Val	Met	Pro	Thr	Gly	Gly	Lys	Ser	Leu	Cys	Tyr	Gln	Ile	Pro	
				35				40					45	
Ala	Leu	Leu	Leu	Asn	Gly	Leu	Thr	Val	Val	Val	Ser	Pro	Leu	Ile
				50				55					60	
Ser	Leu	Met	Lys	Asp	Gln	Val	Asp	Gln	Leu	Gln	Ala	Asn	Gly	Val
				65				70					75	
Ala	Ala	Ala	Cys	Leu	Asn	Ser	Thr	Gln	Thr	Arg	Glu	Gln	Gln	Leu
				80				85					90	
Glu	Val	Met	Thr	Gly	Cys	Arg	Thr	Gly	Gln	Ile	Arg	Leu	Leu	Tyr
				95				100					105	
Ile	Ala	Pro	Glu	Arg	Leu	Met	Leu	Asp	Asn	Phe	Leu	Glu	His	Leu
				110				115					120	
Ala	His	Trp	Asn	Pro	Val	Leu	Leu	Ala	Val	Asp	Glu	Ala	His	Cys
				125				130					135	
Ile	Ser	Gln	Trp	Gly	His	Asp	Phe	Arg	Pro	Glu	Tyr	Ala	Ala	Leu
				140				145					150	
Gly	Gln	Leu	Arg	Gln	Arg	Phe	Pro	Thr	Leu	Pro	Phe	Met	Ala	Leu
				155				160					165	
Thr	Ala	Thr	Ala	Asp	Asp	Thr	Thr	Arg	Gln	Asp	Ile	Val	Arg	Leu
				170				175					180	
Leu	Gly	Leu	Asn	Asp	Pro	Leu	Ile	Gln	Ile	Ser	Ser	Phe	Asp	Arg
				185				190					195	
Pro	Asn	Ile	Arg	Tyr	Met	Leu	Met	Glu	Lys	Phe	Lys	Pro	Leu	Asp

200	205	210
Gln Leu Met Arg Tyr Val Gln Glu Gln Arg Gly Lys Ser Gly Ile		
215	220	225
Ile Tyr Cys Asn Ser Arg Ala Lys Val Glu Asp Thr Ala Ala Ala		
230	235	240
Leu Gln Ser Lys Gly Ile Ser Ala Ala Ala Tyr His Ala Gly Leu		
245	250	255
Glu Asn Asn Val Arg Ala Asp Val Gln Glu Lys Phe Gln Arg Asp		
260	265	270
Asp Leu Gln Ile Val Val Ala Thr Val Ala Phe Gly Met Gly Ile		
275	280	285
Asn Lys Pro Asn Val Arg Phe Val Val His Phe Asp Ile Pro Arg		
290	295	300
Asn Ile Glu Ser Tyr Tyr Gln Glu Thr Gly Arg Ala Gly Arg Asp		
305	310	315
Gly Leu Pro Ala Glu Ala Met Leu Phe Tyr Asp Pro Ala Asp Met		
320	325	330
Ala Trp Leu Arg Arg Cys Leu Glu Glu Lys Pro Gln Gly Gln Leu		
335	340	345
Gln Asp Ile Glu Arg His Lys Leu Asn Ala Met Gly Ala Phe Ala		
350	355	360
Glu Ala Gln Thr Cys Arg Arg Leu Val Leu		
365	370	

(79) INFORMATION FOR SEQ ID NO: 78

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1417
  - (B) TYPE: AMINO ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE:
  - (A) DESCRIPTION: OTHER NUCLEIC ACID
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78

Met Ala Ala Val Pro Gln Asn Asn Leu Gln Glu Gln  
1 5 10

Leu Glu Arg His Ser Ala Arg Thr Leu Asn Asn Lys Leu Ser Leu Ser  
15 20 25

Lys Pro Lys Phe Ser Gly Phe Thr Phe Lys Lys Lys Thr Ser Ser Asp  
30 35 40

Asn Asn Val Ser Val Thr Asn Val Ser Val Ala Lys Thr Pro Val Leu  
45 50 55 60

Arg Asn Lys Asp Val Asn Val Thr Glu Asp Phe Ser Phe Ser Glu Pro  
65 70 75

Leu Pro Asn Thr Thr Asn Gln Gln Arg Val Lys Asp Phe Phe Lys Asn  
80 85 90

Ala Pro Ala Gly Gln Glu Thr Gln Arg Gly Gly Ser Lys Ser Leu Leu  
95 100 105

Pro Asp Phe Leu Gln Thr Pro Lys Glu Val Val Cys Thr Thr Gln Asn  
110 115 120

Thr Pro Thr Val Lys Lys Ser Arg Asp Thr Ala Leu Lys Lys Leu Glu  
125 130 135 140

Phe Ser Ser Ser Pro Asp Ser Leu Ser Thr Ile Asn Asp Trp Asp Asp  
145 150 155

Met Asp Asp Phe Asp Thr Ser Glu Thr Ser Lys Ser Phe Val Thr Pro  
160 165 170

Pro Gln Ser His Phe Val Arg Val Ser Thr Ala Gln Lys Ser Lys Lys  
175 180 185

Gly Lys Arg Asn Phe Phe Lys Ala Gln Leu Tyr Thr Thr Asn Thr Val  
190 195 200

Lys Thr Asp Leu Pro Pro Pro Ser Ser Glu Ser Glu Gln Ile Asp Leu  
205 210 215 220

Thr Glu Glu Gln Lys Asp Asp Ser Glu Trp Leu Ser Ser Asp Val Ile  
225 230 235

Cys Ile Asp Asp Gly Pro Ile Ala Glu Val His Ile Asn Glu Asp Ala  
240 245 250

Gln Glu Ser Asp Ser Leu Lys Thr His Leu Glu Asp Glu Arg Asp Asn  
255 260 265

Ser Glu Lys Lys Asn Leu Glu Glu Ala Glu Leu His Ser Thr Glu  
270 275 280

Lys Val Pro Cys Ile Glu Phe Asp Asp Asp Tyr Asp Thr Asp Phe  
285 290 295 300

Val Pro Pro Ser Pro Glu Glu Ile Ile Ser Ala Ser Ser Ser Ser  
305 310 315

Lys Cys Leu Ser Thr Leu Lys Asp Leu Asp Thr Ser Asp Arg Lys Glu  
320 325 330

Asp Val Leu Ser Thr Ser Lys Asp Leu Leu Ser Lys Pro Glu Lys Met  
335 340 345

Ser Met Gln Glu Leu Asn Pro Glu Thr Ser Thr Asp Cys Asp Ala Arg  
350 355 360

Gln Ile Ser Leu Gln Gln Leu Ile His Val Met Glu His Ile Cys  
365 370 375 380

Lys Leu Ile Asp Thr Ile Pro Asp Asp Lys Leu Lys Leu Asp Cys  
385 390 395

Gly Asn Glu Leu Leu Gln Gln Arg Asn Ile Arg Arg Lys Leu Leu Thr  
400 405 410

Glu Val Asp Phe Asn Lys Ser Asp Ala Ser Leu Leu Gly Ser Leu Trp  
415 420 425

Arg Tyr Arg Pro Asp Ser Leu Asp Gly Pro Met Glu Gly Asp Ser Cys  
430 435 440

Pro Thr Gly Asn Ser Met Lys Glu Leu Asn Phe Ser His Leu Pro Ser  
445 450 455 460

Asn Ser Val Ser Pro Gly Asp Cys Leu Leu Thr Thr Thr Leu Gly Lys  
465 470 475

Thr Gly Phe Ser Ala Thr Arg Lys Asn Leu Phe Glu Arg Pro Leu Phe  
480 485 490

Asn Thr His Leu Gln Lys Ser Phe Val Ser Ser Asn Trp Ala Glu Thr

495	500	505
Pro Arg Leu Gly Lys Lys Asn Glu Ser Ser Tyr Phe Pro Gly Asn Val		
510	515	520
Leu Thr Ser Thr Ala Val Lys Asp Gln Asn Lys His Thr Ala Ser Ile		
525	530	535
540		
Asn Asp Leu Glu Arg Glu Thr Gln Pro Ser Tyr Asp Ile Asp Asn Phe		
545	550	555
Asp Ile Asp Asp Phe Asp Asp Asp Asp Trp Glu Asp Ile Met His		
560	565	570
Asn Leu Ala Ala Ser Lys Ser Ser Thr Ala Ala Tyr Gln Pro Ile Lys		
575	580	585
Glu Gly Arg Pro Ile Lys Ser Val Ser Glu Arg Leu Ser Ser Ala Lys		
590	595	600
Thr Asp Cys Leu Pro Val Ser Ser Thr Ala Gln Asn Ile Asn Phe Ser		
605	610	615
620		
Glu Ser Ile Gln Asn Tyr Thr Asp Lys Ser Ala Gln Asn Leu Ala Ser		
625	630	635
Arg Asn Leu Lys His Glu Arg Phe Gln Ser Leu Ser Phe Pro His Thr		
640	645	650
Lys Glu Met Met Lys Ile Phe His Lys Lys Phe Gly Leu His Asn Phe		
655	660	665
Arg Thr Asn Gln Leu Glu Ala Ile Asn Ala Ala Leu Leu Gly Glu Asp		
670	675	680
Cys Phe Ile Leu Met Pro Thr Gly Gly Lys Ser Leu Cys Tyr Gln		
685	690	695
700		
Leu Pro Ala Cys Val Ser Pro Gly Val Thr Val Val Ile Ser Pro Leu		
705	710	715
Arg Ser Leu Ile Val Asp Gln Val Gln Lys Leu Thr Ser Leu Asp Ile		
720	725	730
Pro Ala Thr Tyr Leu Thr Gly Asp Lys Thr Asp Ser Glu Ala Thr Asn		
735	740	745
Ile Tyr Leu Gln Leu Ser Lys Lys Asp Pro Ile Ile Lys Leu Leu Tyr		
750	755	760
Val Thr Pro Glu Lys Ile Cys Ala Ser Asn Arg Leu Ile Ser Thr Leu		
765	770	775
780		

Glu Asn Leu Tyr Glu Arg Lys Leu Leu Ala Arg Phe Val Ile Asp Glu  
785 790 795

Ala His Cys Val Ser Gln Trp Gly His Asp Phe Arg Gln Asp Tyr Lys  
800 805 810

Arg Met Asn Met Leu Arg Gln Lys Phe Pro Ser Val Pro Val Met Ala  
815 820 825

Leu Thr Ala Thr Ala Asn Pro Arg Val Gln Lys Asp Ile Leu Thr Gln  
830 835 840

Leu Lys Ile Leu Arg Pro Gln Val Phe Ser Met Ser Phe Asn Arg His  
845 850 855 860

Asn Leu Lys Tyr Tyr Val Leu Pro Lys Lys Pro Lys Lys Val Ala Phe  
865 870 875

Asp Cys Leu Glu Trp Ile Arg Lys His His Pro Tyr Asp Ser Gly Ile  
880 885 890

Ile Tyr Cys Leu Ser Arg Arg Glu Cys Asp Thr Met Ala Asp Thr Leu  
895 900 905

Gln Arg Asp Gly Leu Ala Ala Leu Ala Tyr His Ala Gly Leu Ser Asp  
910 915 920

Ser Ala Arg Asp Glu Val Gln Gln Lys Trp Ile Asn Gln Asp Gly Cys  
925 930 935 940

Gln Val Ile Cys Ala Thr Ile Ala Phe Gly Met Gly Ile Asp Lys Pro  
945 950 955

Asp Val Arg Phe Val Ile His Ala Ser Leu Pro Lys Ser Val Glu Gly  
960 965 970

Tyr Tyr Gln Glu Ser Gly Arg Ala Gly Arg Asp Gly Glu Ile Ser His  
975 980 985

Cys Leu Leu Phe Tyr Thr Tyr His Asp Val Thr Arg Leu Lys Arg Leu  
990 995 1000

Ile Met Met Glu Lys Asp Gly Asn His His Thr Arg Glu Thr His Phe  
1005 1010 1015 1020

Asn Asn Leu Tyr Ser Met Val His Tyr Cys Glu Asn Ile Thr Glu Cys  
1025 1030 1035

Arg Arg Ile Gln Leu Leu Ala Tyr Phe Gly Glu Asn Gly Phe Asn Pro  
1040 1045 1050

Asp Phe Cys Lys Lys His Pro Asp Val Ser Cys Asp Asn Cys Cys Lys  
1055 1060 1065

Thr Lys Asp Tyr Lys Thr Arg Asp Val Thr Asp Asp Val Lys Ser Ile  
1070 1075 1080

Val Arg Phe Val Gln Glu His Ser Ser Ser Gln Gly Met Arg Asn Ile  
1085 1090 1095 1100

Lys His Val Gly Pro Ser Gly Arg Phe Thr Met Asn Met Leu Val Asp  
1105 1110 1115

Ile Phe Leu Gly Ser Lys Ser Ala Lys Ile Gln Ser Gly Ile Phe Gly  
1120 1125 1130

Lys Gly Ser Ala Tyr Ser Arg His Asn Ala Glu Arg Leu Phe Lys Lys  
1135 1140 1145

Leu Ile Leu Asp Lys Ile Leu Asp Glu Asp Leu Tyr Ile Asn Ala Asn  
1150 1155 1160

Asp Gln Ala Ile Ala Tyr Val Met Leu Gly Asn Lys Ala Gln Thr Val  
1165 1170 1175 1180

Leu Asn Gly Asn Leu Lys Val Asp Phe Met Glu Thr Glu Asn Ser Ser  
1185 1190 1195

Ser Val Lys Lys Gln Lys Ala Leu Val Ala Lys Val Ser Gln Arg Glu  
1200 1205 1210

Glu Met Val Lys Lys Cys Leu Gly Glu Leu Thr Glu Val Cys Lys Ser  
1215 1220 1225

Leu Gly Lys Val Phe Gly Val His Tyr Phe Asn Ile Phe Asn Thr Val  
1230 1235 1240

Thr Leu Lys Lys Leu Ala Glu Ser Leu Ser Ser Asp Phe Glu Val Leu  
1245 1250 1255 1260

Leu Gln Ile Asp Gly Val Thr Glu Asp Lys Leu Glu Lys Tyr Gly Ala  
1265 1270 1275

Glu Val Ile Ser Val Leu Gln Lys Tyr Ser Glu Trp Thr Ser Pro Ala  
1280 1285 1290

Glu Asp Ser Ser Pro Gly Ile Ser Leu Ser Ser Arg Gly Pro Gly  
1295 1300 1305

Arg Ser Ala Ala Glu Glu Leu Asp Glu Glu Ile Pro Val Ser Ser His  
1310 1315 1320

Tyr Phe Ala Ser Lys Thr Arg Asn Glu Arg Lys Arg Lys Lys Met Pro  
1325 1330 1335 1340  
Ala Ser Gln Arg Ser Lys Arg Arg Lys Thr Ala Ser Ser Gly Ser Lys  
1345 1350 1355  
Ala Lys Gly Gly Ser Ala Thr Cys Arg Lys Ile Ser Ser Lys Thr Lys  
1360 1365 1370  
Ser Ser Ser Ile Ile Gly Ser Ser Ala Ser His Thr Ser Gln Ala  
1375 1380 1385  
Thr Ser Gly Ala Asn Ser Lys Leu Gly Ile Met Ala Pro Pro Lys Pro  
1390 1395 1400  
Ile Asn Arg Pro Phe Leu Lys Pro Ser Tyr Ala Phe Ser  
1405 1410 1415